The following Listing of the Claims replaces all prior versions and all prior listings of the claims in the present application:

Listing of the Claims

- 1. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of determine the presence of a microbe inhabiting in a host organism, comprising the steps of:
 - a) obtaining sequence information from a plurality of sequences from a host organism; and
 - b) searching a database of host organism genomic sequences to determine the presence or absence of said plurality of sequences in said database, wherein a sequence is present in said database if it contains 20 consecutive nucleotides of sequence identical to a sequence in said database, wherein the absence of at least one of said sequences in said database indicates that said at least one sequence is a candidate microbial sequence wherein the absence of said candidate microbial sequence in said database is indicative of belonging to a microbe, thereby indicating the presence of a microbe inhabiting in said host organism.
- 2. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of determine the presence of a microbe inhabiting in a host organism, comprising the steps of:
 - a) obtaining sequence information from a library of genomic DNA from a host organism suspected of harboring a microbe; and
 - b) searching a database of host organism genomic sequences from host organisms which do not harbor the microbe to determine the presence or absence of a sequence in said library in said database, wherein a sequence

is present in said database if it contains 20 consecutive nucleotides of sequence identical to a sequence in said database; wherein the absence of said sequence indicates that said sequence is a candidate microbe sequence, thereby indicating which is indicative of the presence of a microbe inhabiting in said host organism.

- 3. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of determine the presence of a microbe inhabiting in a host organism, comprising the steps of:
 - a) obtaining sequence information from a plurality of expressed sequences from a host organism; and
 - b) searching a database of host organism genomic sequences to determine the presence or absence of said plurality of expressed sequences in said database, wherein a sequence is present in said database if it contains 20 consecutive nucleotides of sequence identical to a sequence in said database and wherein the absence of at least one of said expressed sequences in said database indicates that said at least one sequence is a candidate sequence belonging to a microbe, thereby indicating which is indicative of the presence of a microbe inhabiting in said host organism.
- 4. (Currently Amended) The method according to claims 1, 2, or 3, <u>further comprising the</u>
 <u>step of comparing said candidate sequence to a database of microbial sequences, wherein</u>
 <u>the presence of a said candidate sequence in said database of microbial sequences</u>
 <u>identifies said candidate sequence as belonging wherein said candidate sequence belongs</u>
 to a <u>symbiotice</u> microbial organism.
- 5. (Currently Amended) The method according to claim 4, wherein said candidate sequence belongs to microbial organism is a mutualistic organism, a commensal organism, or a parasitic organism or a pathogenic organism.

6. (Currently Amended) The method according to claim 1, 2 or 3 4, wherein said candidate sequence belongs to host organism in step (a) has a pathogenic condition and said microbial organism is an intracellular a pathogenic organism.

- 7. (Currently Amended) The method according claims 1, 2, or 3, wherein said plurality of sequences are compared to said database of host genomic sequences simultaneously.
- 8. (Currently Amended) The method of claims 1, 2 or 3 wherein said host organism in step

 (a) has a pathogenic condition, and wherein said microbe is an intracellular pathogen

 microbe inhabiting a host organism is an intracellular pathogen, wherein said host

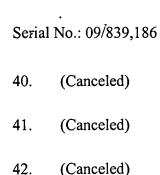
 organism in step (a) has a pathogenic condition, and wherein said database of host

 organism genomic sequences in step (b) comprises genomic sequences of a plurality of
 host organisms not having said pathogenic condition.
- 9. (Previously Presented) The method according to claim 8, wherein said plurality of sequences are compared simultaneously with sequences in said database of host genomic sequences.
- 10. (Previously Presented) The method according to claim 1, wherein said sequences of said plurality of sequences are expressed sequences.
- 11. (Previously Presented) The method according to claim 3 or claim 10, wherein said expressed sequences are EST sequences.
- 12. (Previously Presented) The method according to claim 3 or claim 10, wherein said expressed sequences are cDNA sequences.
- 13. (Previously Presented) The method according to claim 1, 2, or 3, wherein said host organism is an animal.
- 14. (Original) The method according to claim 13, wherein said animal is a mammal.
- 15. (Original) The method according to claim 14, wherein said mammal is a human.

- 16. (Original) The method according to claim 13, wherein said animal is an insect, bird, or a fish.
- 17. (Currently Amended) The method according to claim 1, 2, or 3, wherein said host organism is a microorganism, a fungus, or a plant.
- 18. (Original) The method according to claim 11, wherein said candidate sequence is identified by comparing sequences in a database of expressed sequences with said sequences in said genomic database.
- 19. (Previously Presented) The method according to claim 3 or claim 10, wherein said expressed sequences are identified using a differential gene expression assay.
- 20. (Original) The method according to claim 19, wherein said differential gene expression assay is selected from the group consisting of SAGE, cDNA representational difference analysis, and suppression subtraction analysis.
- 21. (Currently Amended) The method according to claim 3 or claim 10, wherein said sequence information from a plurality of expressed sequences comprises sequences candidate sequence is identified using a subtractive hybridization method.
- 22. (Original) The method according to claim 21, wherein said subtractive hybridization method is representational difference analysis.
- 23. (Currently Amended) The method according to claim 1, 2, or 3, <u>further comprising the step of using wherein</u> said candidate sequence is used as a query sequence to search a database of microbial sequences, wherein the presence of said candidate sequence in said <u>database of microbial sequences identifies said candidate sequence as a microbial sequence</u>.
- 24. (Original) The method according to claim 23, wherein said microbial sequences include viral sequences.
- 25. (Previously Presented) The method according to claim 1, 2, or 3, wherein any of: vector sequences, repetitive sequences, mitochondrial sequences, non-host species sequences,

known host organism sequences, and combinations thereof are eliminated from the genomic database comprising sequences from the host organism.

- 26. (Previously Presented) The method according to claim 1, 2, or 3, wherein said searching is performed iteratively using progressively smaller word sizes.
- 27. (Canceled)
- 28. (Canceled)
- 29. (Previously Presented) The method according to claim 6, wherein said pathogen is an infectious disease organism.
- 30. (Previously Presented) The method according to claim 6, wherein said pathogen is associated with a pathogenic condition selected from the group consisting of an inflammatory disease, an autoimmune disease, and a cell proliferative disease.
- 31. (Original) The method according to claim 30, wherein said disease is selected from the group consisting of sarcoidosis, inflammatory bowel disease, atherosclerosis, multiple sclerosis, rheumatoid arthritis, type I diabetes mellitus, lupus erythematosus, Hodgkin's disease, and bronchioalveolar carcinoma.
- 32. (Canceled)
- 33. (Canceled)
- 34. (Canceled)
- 35. (Canceled)
- 36. (Canceled)
- 37. (Canceled)
- 38. (Canceled)
- 39. (Canceled)



- 43. (Canceled)
- 44. (Canceled)
- 45. (Canceled)
- 46. (Canceled)
- 47. (Canceled)
- 48. (Canceled)
- 49. (Canceled)
- 50. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of determine the presence of a microbe inhabiting in a host organism, comprising the steps of:

searching a database of host organism genomic sequences to determine the presence or absence of the plurality of expressed sequences in the database, wherein a sequence is present in said database if it contains 20 consecutive nucleotides of sequence identical to a sequence in said database, wherein the absence of an expressed sequence in the database identifies the expressed sequence as a candidate microbial microbe sequence, wherein the absence of said candidate microbial sequence in said database is indicative of thereby indicating the presence of a microbe inhabiting in said host organism.

51. (Original) The method according to claim 50, wherein said plurality of sequences are from a library of sequences.

- 52. (Canceled)
- 53. (Canceled)
- 54. (Currently Amended) The method according to claim 53 51, wherein said library comprises human sequences from one or more humans having a pathological condition.
- 55. (Original) The method according to claim 54, wherein said pathological condition is a disease selected from the group consisting of an inflammatory disease, an autoimmune disease, and a cell proliferative disease.
- 56. (Original) The method according to claim 55, wherein said disease is selected from the group consisting of sarcoidosis, inflammatory bowel disease, atherosclerosis, multiple sclerosis, rheumatoid arthritis, type I diabetes mellitus, lupus erythematosus, Hodgkin's disease, and bronchioalveolar carcinoma.
- 57. (Original) The method according to claim 50, wherein said step of obtaining sequence information comprises sequencing expressed sequences cloned in a library of expressed sequences.
- 58. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of determine the presence of a microbe inhabiting in a host organism, comprising the steps of:

obtaining expressed sequence information from a plurality of sequences from at least one non-microbial host organism; and

searching a database of microbial sequences from a library of expressed sequences to determine the presence or absence of said plurality of sequences from at least one non-microbial host organism in the database, wherein a sequence is present in said database if it contains 20 consecutive nucleotides of

sequence identical to a sequence in said database, wherein the presence of an expressed sequence from said at least one non-microbial host organism in the database identifies the expressed sequence as a candidate microbe sequence, wherein the presence of said candidate microbial sequence in said database is indicative of thereby indicating the presence of a microbe inhabiting in said host organism.

- 59. (Canceled)
- 60. (Original) The method according to claim 58, wherein said library of expressed sequences comprises sequences from one or more humans having a pathological condition.
- 61. (Original) The method according to claim 60, wherein said pathological condition is an infectious disease.
- 62. (Previously Presented) The method according to claim 8, wherein said pathogen is an infectious disease organism.
- 63. (Previously Presented) The method according to claim 8, wherein said pathogen is associated with a pathogenic condition selected from the group consisting of an inflammatory disease, an autoimmune disease, and a cell proliferative disease.
- 64. (Previously Presented) The method according to claim 63, wherein said disease is selected from the group consisting of sarcoidosis, inflammatory bowel disease, atherosclerosis, multiple sclerosis, rheumatoid arthritis, type I diabetes mellitus, lupus erythematosus, Hodgkin's disease, and bronchioalveolar carcinoma.